



SEQUENCE LISTING

<110> HUGANIR, RICHARD L.
KIM, GJEEHAE

<120> SIGNAL TRANSDUCING SYNAPTIC MOLECULES AND USES THEREOF

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<140> 09/294,298

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<150> 60/082,690

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<170> PatentIn Ver. 2.1

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Thr Gln Tyr Val His Ser Pro Tyr Asp Arg Pro Gly Trp Asn Pro Arg
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Phe Cys Ile Ile Ser Gly Asn Gln Leu Leu Met Leu Asp Glu Asp Glu
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Ile His Pro Leu Leu Ile Arg Asp Arg Arg Ser Glu Ser Ser Arg Asn
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Gly Glu His Glu Tyr His Leu Gly Arg Ser Arg Arg Lys Ser Val Pro	
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Gly Gly Lys Gln Tyr Ser Met Glu Ala Ala Pro Ala Ala Pro Phe Arg	
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 SYNGAP-A

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 Lys Leu Leu Arg Arg Thr Val Ser Val Pro Val Glu Gly Arg Pro His
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 Gly Glu His Glu Tyr His Leu Gly Arg Ser Arg Arg Lys Ser Val Pro
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 Gly Gly Lys Gln Tyr Ser Met Glu Ala Ala Pro Ala Ala Pro Phe Arg
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 Pro Ser Gln Gly Phe Leu Ser Arg Arg Leu Lys Ser Ser Ile Lys Arg
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 Thr Lys Ser Gln Pro Lys Leu Asp Arg Thr Ser Ser Phe Arg Gln Ile
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 Ser Phe Lys Glu Ser His Ser His Glu Ser Leu Leu Ser Pro Ser Ser
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 Pro Val His Ser Ser Ile Leu Gly Gln Glu Phe Cys Phe Glu Val Thr
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 Thr Ser Ser Gly Thr Lys Cys Phe Ala Cys Arg Ser Ala Ala Glu Arg
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 Asp Lys Trp Ile Glu Asn Leu Gln Arg Ala Val Lys Pro Asn Lys Asp
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 Asn Ser Arg Arg Val Asp Asn Val Leu Lys Leu Trp Ile Ile Glu Ala
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Arg Glu Leu Pro Pro Lys Lys Arg Tyr Tyr Cys Glu Leu Cys Leu Asp
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 Asp Thr Val Phe Trp Gly Glu His Phe Glu Phe Asn Asn Leu Pro Ala
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 Val Arg Ala Leu Arg Leu His Leu Tyr Arg Asp Ser Asp Lys Lys Arg
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 Thr Leu Ala Gly Arg His Phe Thr Glu Gln Trp Tyr Pro Val Thr Leu
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 Leu Tyr Lys Glu Phe Ala Glu Tyr Val Thr Asn His Tyr Arg Met Leu
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 Glu Phe Ile Arg Ala Leu Tyr Glu Ser Glu Glu Asn Cys Glu Val Asp
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<213> Unknown Organism

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<223> Description of Unknown Organism: mammalian
SYNGAP-B

<220>

<221> CDS

<222> (4..3741, 3745..4134)

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tgc ccc ctc ctt ccc acc gcc agc ctc tcc gcc gcc gct gct ctt cct	96
Cys Pro Leu Leu Pro Thr Ala Ser Leu Ser Ala Ala Ala Ala Leu Pro	
20 25 30	
gct gct ttc cgg ggg aat acc act tgg gtc gct cga gga gga aga gtg	144
Ala Ala Phe Arg Gly Asn Thr Thr Trp Val Ala Arg Gly Gly Arg Val	
35 40 45	
tcc ccg ggg ggg aaa cag tac agc atg gaa gcc gcc ccc gct gcg ccc	192
Ser Pro Gly Gly Lys Gln Tyr Ser Met Glu Ala Ala Pro Ala Ala Pro	
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ttc cgg ccc tcg caa ggc ttc ctg agc cgg agg cta aaa agc tcc atc	240
Phe Arg Pro Ser Gln Gly Phe Leu Ser Arg Arg Leu Lys Ser Ser Ile	
65 70 75	
aaa cgt aca aag tca caa ccc aaa ctt gac cgg acc agc agc ttt cga	288
Lys Arg Thr Lys Ser Gln Pro Lys Leu Asp Arg Thr Ser Ser Phe Arg	
80 85 90 95	
cag atc ctg cct cgc ttc cga agt gct gac cat gac cgg gcc cgg ctg	336
Gln Ile Leu Pro Arg Phe Arg Ser Ala Asp His Asp Arg Ala Arg Leu	
100 105 110	
atg cag agc ttc aag gag tct cac tcc cat gag tcc ctg ctg agt ccc	384
Met Gln Ser Phe Lys Glu Ser His Ser His Glu Ser Leu Leu Ser Pro	
115 120 125	
agc agt gct gct gag gcc ctg gag ctc aac ctg gat gaa gac tcc att	432
Ser Ser Ala Ala Glu Ala Leu Glu Leu Asn Leu Asp Glu Asp Ser Ile	
130 135 140	
atc aag cca gta cac agc tcc atc ctg ggc cag gag ttc tgc ttt gag	480
Ile Lys Pro Val His Ser Ser Ile Leu Gly Gln Glu Phe Cys Phe Glu	
145 150 155	
gta aca aca tcg tct ggg aca aaa tgt ttt gcc tgt cgg tct gca gcc	528
Val Thr Thr Ser Ser Gly Thr Lys Cys Phe Ala Cys Arg Ser Ala Ala	
160 165 170 175	
gaa agg gac aaa tgg att gag aat cta cag agg gct gtg aaa ccc aac	576
Glu Arg Asp Lys Trp Ile Glu Asn Leu Gln Arg Ala Val Lys Pro Asn	
180 185 190	
aag gac aac agc cgc cgg gta gat aac gtg ctg aaa cta tgg atc ata	624
Lys Asp Asn Ser Arg Arg Val Asp Asn Val Leu Lys Leu Trp Ile Ile	
195 200 205	

gaa gct cga gag ctg ccc ccc aag aag cga tat tac tgc gag tta tgc	672
Glu Ala Arg Glu Leu Pro Pro Lys Lys Arg Tyr Tyr Cys Glu Leu Cys	
210 215 220	
ctg gac gac atg ctc tat gca cgg acc act tcc aag ccc cgc tca gcc	720
Leu Asp Asp Met Leu Tyr Ala Arg Thr Thr Ser Lys Pro Arg Ser Ala	
225 230 235	
tca gga gac act gtc ttt tgg ggc gag cac ttc gag ttt aac aac ctg	768
Ser Gly Asp Thr Val Phe Trp Gly Glu His Phe Glu Phe Asn Asn Leu	
240 245 250 255	
cct gct gtc cgg gcg ctg cgg ctg cat ctg tac cgt gac tgc gac aaa	816
Pro Ala Val Arg Ala Leu Arg Leu His Leu Tyr Arg Asp Ser Asp Lys	
260 265 270	
aag cgg aag aag gac aag gca ggc tac gtt ggc ctg gtg act gtt cca	864
Lys Arg Lys Lys Asp Lys Ala Gly Tyr Val Gly Leu Val Thr Val Pro	
275 280 285	
gtg gcc acc ctg gct ggg cgc cac ttc aca gag cag tgg tac ccc gtg	912
Val Ala Thr Leu Ala Gly Arg His Phe Thr Glu Gln Trp Tyr Pro Val	
290 295 300	
acc ctg cca aca gga agt ggg ggc tct ggg ggt atg ggc tgc ggg gga	960
Thr Leu Pro Thr Gly Ser Gly Gly Ser Gly Gly Met Gly Ser Gly Gly	
305 310 315	
gga ggg ggg tca ggg ggc ggc tca ggg ggc aaa ggg aaa gga ggc tgt	1008
Gly Gly Gly Ser Gly Gly Gly Ser Gly Gly Lys Gly Lys Gly Gly Cys	
320 325 330 335	
cct gct gtg cgg ctg aag gcc cgt tac cag aca atg agt atc ctg ccc	1056
Pro Ala Val Arg Leu Lys Ala Arg Tyr Gln Thr Met Ser Ile Leu Pro	
340 345 350	
atg gag cta tat aag gag ttt gca gaa tat gtg acc aac cac tac cgc	1104
Met Glu Leu Tyr Lys Glu Phe Ala Glu Tyr Val Thr Asn His Tyr Arg	
355 360 365	
atg ctg tgt gcc gtg ctg gag ccc gcc ctc aat gtc aag ggc aag gag	1152
Met Leu Cys Ala Val Leu Glu Pro Ala Leu Asn Val Lys Gly Lys Glu	
370 375 380	
gag gtc gct agt gca ctg gtt cac atc ctg caa agc aca ggc aag gcc	1200
Glu Val Ala Ser Ala Leu Val His Ile Leu Gln Ser Thr Gly Lys Ala	
385 390 395	
aag gac ttc ctt tca gac atg gcc atg tca gag gta gac cgg ttc atg	1248
Lys Asp Phe Leu Ser Asp Met Ala Met Ser Glu Val Asp Arg Phe Met	
400 405 410 415	
gag cgg gaa cac ctc ata ttc cgc gag aac acg ctc gcc act aaa gcc	1296
Glu Arg Glu His Leu Ile Phe Arg Glu Asn Thr Leu Ala Thr Lys Ala	
420 425 430	

ata gaa gag tat atg aga ctg att ggc cag aaa tac ctc aag gat gcc Ile Glu Glu Tyr Met Arg Leu Ile Gly Gln Lys Tyr Leu Lys Asp Ala 435 440 445	1344
att ggg gag ttc atc cgg gct ctg tat gaa tct gag gag aac tgt gaa Ile Gly Glu Phe Ile Arg Ala Leu Tyr Glu Ser Glu Glu Asn Cys Glu 450 455 460	1392
gta gac ccc atc aag tgc aca gcg tcc agt ctg gca gag cac cag gcc Val Asp Pro Ile Lys Cys Thr Ala Ser Ser Leu Ala Glu His Gln Ala 465 470 475	1440
aac ctg cgg atg tgc tgt gag ttg gcc ctg tgc aag gtg gtc aac tcc Asn Leu Arg Met Cys Cys Glu Leu Ala Leu Cys Lys Val Val Asn Ser 480 485 490 495	1488
cat tgc gtg ttc ccg agg gag ctg aag gag gtg ttt gca tca tgg cgg His Cys Val Phe Pro Arg Glu Leu Lys Glu Val Phe Ala Ser Trp Arg 500 505 510	1536
ctg cgc tgt gca gag cgg ggc cgg gag gac att gct gac agg ctg atc Leu Arg Cys Ala Glu Arg Gly Arg Glu Asp Ile Ala Asp Arg Leu Ile 515 520 525	1584
agc gcc tcg ctc ttc ctg cgc ttc ctc tgc ccg gcc atc atg tcg ccc Ser Ala Ser Leu Phe Leu Arg Phe Leu Cys Pro Ala Ile Met Ser Pro 530 535 540	1632
agt ctg ttt gga ctg atg cag gag tac cca gat gag cag acc tca cga Ser Leu Phe Gly Leu Met Gln Glu Tyr Pro Asp Glu Gln Thr Ser Arg 545 550 555	1680
acc ctc acc ctc atc gcc aag gtt atc cag aac ctg gcc aac ttt tcc Thr Leu Thr Leu Ile Ala Lys Val Ile Gln Asn Leu Ala Asn Phe Ser 560 565 570 575	1728
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ctg gac aca ctg acc aac agc agc agt ttt gag ggc tac ata gac ttg Leu Asp Thr Leu Thr Asn Ser Ser Ser Phe Glu Gly Tyr Ile Asp Leu 610 615 620	1872
ggc cgc gag ctc tcc aca ctt cac gcc ctg ctc tgg gag gtg ctg ccc Gly Arg Glu Leu Ser Thr Leu His Ala Leu Leu Trp Glu Val Leu Pro 625 630 635	1920
cag ctc agc aag gaa gcc ctc ctg aag ctg ggc ccg ctg ccc cgg ctc Gln Leu Ser Lys Glu Ala Leu Leu Lys Leu Gly Pro Leu Pro Arg Leu 640 645 650 655	1968

ctc agc gac atc agc aca gcc ctg agg aac cct aac atc caa agg cag Leu Ser Asp Ile Ser Thr Ala Leu Arg Asn Pro Asn Ile Gln Arg Gln 660 665 670	2016
ccg agc cgc cag agc gag cgc gct cgg tct cag ccc atg gtg ctg cgc Pro Ser Arg Gln Ser Glu Arg Ala Arg Ser Gln Pro Met Val Leu Arg 675 680 685	2064
ggg ccg tca gcc gag atg cag ggc tac atg atg cgg gac ctc aac agc Gly Pro Ser Ala Glu Met Gln Gly Tyr Met Met Arg Asp Leu Asn Ser 690 695 700	2112
tcc atc gac ctt cag tcc ttc atg gct cga ggc ctc aac agc tct atg Ser Ile Asp Leu Gln Ser Phe Met Ala Arg Gly Leu Asn Ser Ser Met 705 710 715	2160
gac atg gct cgc ctc ccc tcc cca acc aag gag aaa ccc ccg ccg ccc Asp Met Ala Arg Leu Pro Ser Pro Thr Lys Glu Lys Pro Pro Pro 720 725 730 735	2208
cct ccc ggt ggg ggt aaa gac ctg ttc tat gtg agc cgg cca cca ctg Pro Pro Gly Gly Gly Lys Asp Leu Phe Tyr Val Ser Arg Pro Pro Leu 740 745 750	2256
gcc cgg tcc tcc cca gca tac tgc acg agc agc tcg gac atc aca gag Ala Arg Ser Ser Pro Ala Tyr Cys Thr Ser Ser Ser Asp Ile Thr Glu 755 760 765	2304
ccg gag cag aag atg ctg agt gtc aac aag agt gtg tcc atg ctg gac Pro Glu Gln Lys Met Leu Ser Val Asn Lys Ser Val Ser Met Leu Asp 770 775 780	2352
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aac ctg gca gct gtt ggg gac ctg ttg cac tca agc cag gct tca ctg Asn Leu Ala Ala Val Gly Asp Leu Leu His Ser Ser Gln Ala Ser Leu 800 805 810 815	2448
aca gca gcc ttg ggg ttg cgg cct gca cct gcc ggg cgc ctc tcc caa Thr Ala Ala Leu Gly Leu Arg Pro Ala Pro Ala Gly Arg Leu Ser Gln 820 825 830	2496
ggg agt ggc tct tcc atc aca gca gcc ggc atg cgc ctc agc cag atg Gly Ser Gly Ser Ser Ile Thr Ala Ala Gly Met Arg Leu Ser Gln Met 835 840 845	2544
ggt gtc act acg gat ggt gtc ccc gcc cag caa ctg cgc atc cct ctt Gly Val Thr Thr Asp Gly Val Pro Ala Gln Gln Leu Arg Ile Pro Leu 850 855 860	2592
tcc ttc cag aac cct ctc ttc cat atg gct gcc gat gga cca ggg ccc Ser Phe Gln Asn Pro Leu Phe His Met Ala Ala Asp Gly Pro Gly Pro 865 870 875	2640

cca gca ggc cat gga ggg agc agt ggc cat ggt cca cct tcc tcc cat Pro Ala Gly His Gly Gly Ser Ser Gly His Gly Pro Pro Ser Ser His 880 885 890 895	2688
cac cac cac cac cac cat cac cat cac cga ggg gga gaa ccc cca ggg His His His His His His His His His Arg Gly Gly Glu Pro Pro Gly 900 905 910	2736
gac act ttt gcc ccg ttc cat ggc tat agc aag agc gag gac ctc tct Asp Thr Phe Ala Pro Phe His Gly Tyr Ser Lys Ser Glu Asp Leu Ser 915 920 925	2784
aca ggg gtc cct aag ccc cct gcg gcc tcc atc ctt cac agc cac agc Thr Gly Val Pro Lys Pro Pro Ala Ala Ser Ile Leu His Ser His Ser 930 935 940	2832
tac agt gat gag ttt gga ccc tct ggt act gat ttt acc cgt cgg cag Tyr Ser Asp Glu Phe Gly Pro Ser Gly Thr Asp Phe Thr Arg Arg Gln 945 950 955	2880
ctc tca ctt cag gac aac cta cag cac atg ctc tcc ccg ccc cag atc Leu Ser Leu Gln Asp Asn Leu Gln His Met Leu Ser Pro Pro Gln Ile 960 965 970 975	2928
acc atc ggt ccc cag agg cca gct ccc tca ggg cca gga ggg ggc agt Thr Ile Gly Pro Gln Arg Pro Ala Pro Ser Gly Pro Gly Gly Gly Ser 980 985 990	2976
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ccg tcc agc ggg aac cta ttg cag tcc ccg gaa cca agt tat ggt cct Pro Ser Ser Gly Asn Leu Leu Gln Ser Pro Glu Pro Ser Tyr Gly Pro 1025 1030 1035	3120
gcc cgt cca cgg caa cag agc ctc agc aaa gag ggc agc att ggg ggc Ala Arg Pro Arg Gln Gln Ser Leu Ser Lys Glu Gly Ser Ile Gly Gly 1040 1045 1050 1055	3168
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gag tac tcg aag tcc atg gac gag agc cga ctg gac agg gtg aag gag Glu Tyr Ser Lys Ser Met Asp Glu Ser Arg Leu Asp Arg Val Lys Glu 1120 1125 1130 1135	3408
tac gag gag gag atc cac tca ctg aag gaa agg cta cac atg tcc aac Tyr Glu Glu Glu Ile His Ser Leu Lys Glu Arg Leu His Met Ser Asn 1140 1145 1150	3456
cgg aag ctg gaa gag tac gag cgg agg ctg ctg tcc cag gaa gag cag Arg Lys Leu Glu Glu Tyr Glu Arg Arg Leu Leu Ser Gln Glu Glu Gln 1155 1160 1165	3504
acc agc aag atc ctg atg cag tac caa gcc cgc ctg gag cag agc gag Thr Ser Lys Ile Leu Met Gln Tyr Gln Ala Arg Leu Glu Gln Ser Glu 1170 1175 1180	3552
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ccc gcc atg gct gag ccg ctg cct gaa ccc aag aag agg ctg ctc gac Pro Ala Met Ala Glu Pro Leu Pro Glu Pro Lys Lys Arg Leu Leu Asp 1220 1225 1230	3696
gct cag aga ggc agc ttc ccc cct tgg gtc caa caa acc cgc gtg Ala Gln Arg Gly Ser Phe Pro Pro Trp Val Gln Gln Thr Arg Val 1235 1240 1245	3741
tga cgc tgg ccc cac ctt gga acg gcc tgg ccc ccc cag ccc cac ccc Arg Trp Pro His Leu Gly Thr Ala Trp Pro Pro Gln Pro His Pro 1250 1255 1260	3789
ccc cac ccc ggc tgc aga tca cag aga acg gcg agt tcc gga aca ccg Pro His Pro Gly Cys Arg Ser Gln Arg Thr Ala Ser Ser Gly Thr Pro 1265 1270 1275	3837
cag acc act agc cca ccc agc atc aca gac ctc ctt ccc tgt gca ccc Gln Thr Thr Ser Pro Pro Ser Ile Thr Asp Leu Leu Pro Cys Ala Pro 1280 1285 1290	3885
tac ccc ggc cca ccc agc gtc aca gac ctc ctt ccc agt gca ccc gac Tyr Pro Gly Pro Pro Ser Val Thr Asp Leu Leu Pro Ser Ala Pro Asp 1295 1300 1305	3933
cct gga aca tca cca acc acc agg act gga cgt cac caa ggg aca gcg Pro Gly Thr Ser Pro Thr Thr Arg Thr Gly Arg His Gln Gly Thr Ala 1310 1315 1320 1325	3981

gga ttg tct ccc tta acg cct cct tgg ggc acc cat ctg tca acc cca 4029
 Gly Leu Ser Pro Leu Thr Pro Pro Trp Gly Thr His Leu Ser Thr Pro
 1330 1335 1340

ctg ctc cat tcc agg agg gag agt ggg acc ctc agc tgc cct ctc acc 4077
 Leu Leu His Ser Arg Arg Glu Ser Gly Thr Leu Ser Cys Pro Leu Thr
 1345 1350 1355

cca gga cac cac cta ccc cac aca gac ccc ttc act ctg ggg tgc tat 4125
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ccc cat cct 4134
 Pro His Pro
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<212> PRT

<213> Unknown Organism

<220>

<223> Description of Unknown Organism: mammalian
 SYNGAP-B

<400> 4

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Ala Phe Arg Gly Asn Thr Thr Trp Val Ala Arg Gly Gly Arg Val Ser
 35 40 45

Pro Gly Gly Lys Gln Tyr Ser Met Glu Ala Ala Pro Ala Ala Pro Phe
 50 55 60

Arg Pro Ser Gln Gly Phe Leu Ser Arg Arg Leu Lys Ser Ser Ile Lys
 65 70 75 80

Arg Thr Lys Ser Gln Pro Lys Leu Asp Arg Thr Ser Ser Phe Arg Gln
 85 90 95

Ile Leu Pro Arg Phe Arg Ser Ala Asp His Asp Arg Ala Arg Leu Met
 100 105 110

Gln Ser Phe Lys Glu Ser His Ser His Glu Ser Leu Leu Ser Pro Ser
 115 120 125

Ser Ala Ala Glu Ala Leu Glu Leu Asn Leu Asp Glu Asp Ser Ile Ile
 130 135 140

Lys Pro Val His Ser Ser Ile Leu Gly Gln Glu Phe Cys Phe Glu Val
 145 150 155 160

Thr Thr Ser Ser Gly Thr Lys Cys Phe Ala Cys Arg Ser Ala Ala Glu
 165 170 175
 Arg Asp Lys Trp Ile Glu Asn Leu Gln Arg Ala Val Lys Pro Asn Lys
 180 185 190
 Asp Asn Ser Arg Arg Val Asp Asn Val Leu Lys Leu Trp Ile Ile Glu
 195 200 205
 Ala Arg Glu Leu Pro Pro Lys Lys Arg Tyr Tyr Cys Glu Leu Cys Leu
 210 215 220
 Asp Asp Met Leu Tyr Ala Arg Thr Thr Ser Lys Pro Arg Ser Ala Ser
 225 230 235 240
 Gly Asp Thr Val Phe Trp Gly Glu His Phe Glu Phe Asn Asn Leu Pro
 245 250 255
 Ala Val Arg Ala Leu Arg Leu His Leu Tyr Arg Asp Ser Asp Lys Lys
 260 265 270
 Arg Lys Lys Asp Lys Ala Gly Tyr Val Gly Leu Val Thr Val Pro Val
 275 280 285
 Ala Thr Leu Ala Gly Arg His Phe Thr Glu Gln Trp Tyr Pro Val Thr
 290 295 300
 Leu Pro Thr Gly Ser Gly Gly Ser Gly Gly Met Gly Ser Gly Gly Gly
 305 310 315 320
 Gly Gly Ser Gly Gly Gly Ser Gly Gly Lys Gly Lys Gly Gly Cys Pro
 325 330 335
 Ala Val Arg Leu Lys Ala Arg Tyr Gln Thr Met Ser Ile Leu Pro Met
 340 345 350
 Glu Leu Tyr Lys Glu Phe Ala Glu Tyr Val Thr Asn His Tyr Arg Met
 355 360 365
 Leu Cys Ala Val Leu Glu Pro Ala Leu Asn Val Lys Gly Lys Glu Glu
 370 375 380
 Val Ala Ser Ala Leu Val His Ile Leu Gln Ser Thr Gly Lys Ala Lys
 385 390 395 400
 Asp Phe Leu Ser Asp Met Ala Met Ser Glu Val Asp Arg Phe Met Glu
 405 410 415
 Arg Glu His Leu Ile Phe Arg Glu Asn Thr Leu Ala Thr Lys Ala Ile
 420 425 430
 Glu Glu Tyr Met Arg Leu Ile Gly Gln Lys Tyr Leu Lys Asp Ala Ile
 435 440 445
 Gly Glu Phe Ile Arg Ala Leu Tyr Glu Ser Glu Glu Asn Cys Glu Val
 450 455 460

Asp	Pro	Ile	Lys	Cys	Thr	Ala	Ser	Ser	Leu	Ala	Glu	His	Gln	Ala	Asn	465	470	475	480
Leu	Arg	Met	Cys	Cys	Glu	Leu	Ala	Leu	Cys	Lys	Val	Val	Asn	Ser	His	485	490	495	
Cys	Val	Phe	Pro	Arg	Glu	Leu	Lys	Glu	Val	Phe	Ala	Ser	Trp	Arg	Leu	500	505	510	
Arg	Cys	Ala	Glu	Arg	Gly	Arg	Glu	Asp	Ile	Ala	Asp	Arg	Leu	Ile	Ser	515	520	525	
Ala	Ser	Leu	Phe	Leu	Arg	Phe	Leu	Cys	Pro	Ala	Ile	Met	Ser	Pro	Ser	530	535	540	
Leu	Phe	Gly	Leu	Met	Gln	Glu	Tyr	Pro	Asp	Glu	Gln	Thr	Ser	Arg	Thr	545	550	555	560
Leu	Thr	Leu	Ile	Ala	Lys	Val	Ile	Gln	Asn	Leu	Ala	Asn	Phe	Ser	Lys	565	570	575	
Phe	Thr	Ser	Lys	Glu	Asp	Phe	Leu	Gly	Phe	Met	Asn	Glu	Phe	Leu	Glu	580	585	590	
Leu	Glu	Trp	Gly	Ser	Met	Gln	Gln	Phe	Leu	Tyr	Glu	Ile	Ser	Asn	Leu	595	600	605	
Asp	Thr	Leu	Thr	Asn	Ser	Ser	Ser	Phe	Glu	Gly	Tyr	Ile	Asp	Leu	Gly	610	615	620	
Arg	Glu	Leu	Ser	Thr	Leu	His	Ala	Leu	Leu	Trp	Glu	Val	Leu	Pro	Gln	625	630	635	640
Leu	Ser	Lys	Glu	Ala	Leu	Leu	Lys	Leu	Gly	Pro	Leu	Pro	Arg	Leu	Leu	645	650	655	
Ser	Asp	Ile	Ser	Thr	Ala	Leu	Arg	Asn	Pro	Asn	Ile	Gln	Arg	Gln	Pro	660	665	670	
Ser	Arg	Gln	Ser	Glu	Arg	Ala	Arg	Ser	Gln	Pro	Met	Val	Leu	Arg	Gly	675	680	685	
Pro	Ser	Ala	Glu	Met	Gln	Gly	Tyr	Met	Met	Arg	Asp	Leu	Asn	Ser	Ser	690	695	700	
Ile	Asp	Leu	Gln	Ser	Phe	Met	Ala	Arg	Gly	Leu	Asn	Ser	Ser	Met	Asp	705	710	715	720
Met	Ala	Arg	Leu	Pro	Ser	Pro	Thr	Lys	Glu	Lys	Pro	Pro	Pro	Pro	Pro	725	730	735	
Pro	Gly	Gly	Gly	Lys	Asp	Leu	Phe	Tyr	Val	Ser	Arg	Pro	Pro	Leu	Ala	740	745	750	
Arg	Ser	Ser	Pro	Ala	Tyr	Cys	Thr	Ser	Ser	Ser	Asp	Ile	Thr	Glu	Pro	755	760	765	

Glu Gln Lys Met Leu Ser Val Asn Lys Ser Val Ser Met Leu Asp Leu
 770 775 780
 Gln Gly Asp Gly Pro Gly Gly Arg Leu Asn Ser Ser Ser Val Ser Asn
 785 790 795 800
 Leu Ala Ala Val Gly Asp Leu Leu His Ser Ser Gln Ala Ser Leu Thr
 805 810 815
 Ala Ala Leu Gly Leu Arg Pro Ala Pro Ala Gly Arg Leu Ser Gln Gly
 820 825 830
 Ser Gly Ser Ser Ile Thr Ala Ala Gly Met Arg Leu Ser Gln Met Gly
 835 840 845
 Val Thr Thr Asp Gly Val Pro Ala Gln Gln Leu Arg Ile Pro Leu Ser
 850 855 860
 Phe Gln Asn Pro Leu Phe His Met Ala Ala Asp Gly Pro Gly Pro Pro
 865 870 875 880
 Ala Gly His Gly Gly Ser Ser Gly His Gly Pro Pro Ser Ser His His
 885 890 895
 His His His His His His His His Arg Gly Gly Glu Pro Pro Gly Asp
 900 905 910
 Thr Phe Ala Pro Phe His Gly Tyr Ser Lys Ser Glu Asp Leu Ser Thr
 915 920 925
 Gly Val Pro Lys Pro Pro Ala Ala Ser Ile Leu His Ser His Ser Tyr
 930 935 940
 Ser Asp Glu Phe Gly Pro Ser Gly Thr Asp Phe Thr Arg Arg Gln Leu
 945 950 955 960
 Ser Leu Gln Asp Asn Leu Gln His Met Leu Ser Pro Pro Gln Ile Thr
 965 970 975
 Ile Gly Pro Gln Arg Pro Ala Pro Ser Gly Pro Gly Gly Gly Ser Gly
 980 985 990
 Gly Gly Ser Gly Gly Gly Gly Gly Gly Gln Pro Pro Pro Leu Gln Arg
 995 1000 1005
 Gly Lys Ser Gln Gln Leu Thr Val Ser Ala Ala Gln Lys Pro Arg Pro
 1010 1015 1020
 Ser Ser Gly Asn Leu Leu Gln Ser Pro Glu Pro Ser Tyr Gly Pro Ala
 1025 1030 1035 1040
 Arg Pro Arg Gln Gln Ser Leu Ser Lys Glu Gly Ser Ile Gly Gly Ser
 1045 1050 1055
 Gly Gly Ser Gly Gly Gly Gly Gly Gly Gly Leu Lys Pro Ser Ile Thr
 1060 1065 1070

Lys Gln His Ser Gln Thr Pro Ser Thr Leu Asn Pro Thr Met Pro Ala
 1075 1080 1085
 Ser Glu Arg Thr Val Ala Trp Val Ser Asn Met Pro His Leu Ser Ala
 1090 1095 1100
 Asp Ile Glu Ser Ala His Ile Glu Arg Glu Glu Tyr Lys Leu Lys Glu
 1105 1110 1115 1120
 Tyr Ser Lys Ser Met Asp Glu Ser Arg Leu Asp Arg Val Lys Glu Tyr
 1125 1130 1135
 Glu Glu Glu Ile His Ser Leu Lys Glu Arg Leu His Met Ser Asn Arg
 1140 1145 1150
 Lys Leu Glu Glu Tyr Glu Arg Arg Leu Leu Ser Gln Glu Glu Gln Thr
 1155 1160 1165
 Ser Lys Ile Leu Met Gln Tyr Gln Ala Arg Leu Glu Gln Ser Glu Lys
 1170 1175 1180
 Arg Leu Arg Gln Gln Gln Val Glu Lys Asp Ser Gln Ile Lys Ser Ile
 1185 1190 1195 1200
 Ile Gly Arg Leu Met Leu Val Glu Glu Glu Leu Arg Arg Asp His Pro
 1205 1210 1215
 Ala Met Ala Glu Pro Leu Pro Glu Pro Lys Lys Arg Leu Leu Asp Ala
 1220 1225 1230
 Gln Arg Gly Ser Phe Pro Pro Trp Val Gln Gln Thr Arg Val Arg Trp
 1235 1240 1245
 Pro His Leu Gly Thr Ala Trp Pro Pro Gln Pro His Pro Pro His Pro
 1250 1255 1260
 Gly Cys Arg Ser Gln Arg Thr Ala Ser Ser Gly Thr Pro Gln Thr Thr
 1265 1270 1275 1280
 Ser Pro Pro Ser Ile Thr Asp Leu Leu Pro Cys Ala Pro Tyr Pro Gly
 1285 1290 1295
 Pro Pro Ser Val Thr Asp Leu Leu Pro Ser Ala Pro Asp Pro Gly Thr
 1300 1305 1310
 Ser Pro Thr Thr Arg Thr Gly Arg His Gln Gly Thr Ala Gly Leu Ser
 1315 1320 1325
 Pro Leu Thr Pro Pro Trp Gly Thr His Leu Ser Thr Pro Leu Leu His
 1330 1335 1340
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 1365 1370 1375

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 <213> Unknown Organism

<220>
 <223> Description of Unknown Organism: mammalian
 SYNGAP-C

<220>
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 1 5 10 15
 cag caa ggc ttc ctg agc cgg agg cta aaa agc tcc atc aaa cgt aca 96
 Gln Gln Gly Phe Leu Ser Arg Arg Leu Lys Ser Ser Ile Lys Arg Thr
 20 25 30
 aag tca caa ccc aaa ctt gac cgg acc agc agc ttt cga cag atc ctg 144
 Lys Ser Gln Pro Lys Leu Asp Arg Thr Ser Ser Phe Arg Gln Ile Leu
 35 40 45
 cct cgc ttc cga agt gct gac cat gac cgg gcc cgg ctg atg cag agc 192
 Pro Arg Phe Arg Ser Ala Asp His Asp Arg Ala Arg Leu Met Gln Ser
 50 55 60
 ttc aag gag tct cac tcc cat gag tcc ctg ctg agt ccc agc agt gct 240
 Phe Lys Glu Ser His Ser His Glu Ser Leu Leu Ser Pro Ser Ser Ala
 65 70 75
 gct gag gcc ctg gag ctc aac ctg gat gaa gac tcc att atc aag cca 288
 Ala Glu Ala Leu Glu Leu Asn Leu Asp Glu Asp Ser Ile Ile Lys Pro
 80 85 90 95
 gta cac agc tcc atc ctg ggc cag gag ttc tgc ttt gag gta aca aca 336
 Val His Ser Ser Ile Leu Gly Gln Glu Phe Cys Phe Glu Val Thr Thr
 100 105 110
 tcg tct ggg aca aaa tgt ttt gcc tgt cgg tct gca gcc gaa agg gac 384
 Ser Ser Gly Thr Lys Cys Phe Ala Cys Arg Ser Ala Ala Glu Arg Asp
 115 120 125
 aaa tgg att gag aat cta cag agg gct gtg aaa ccc aac aag gac aac 432
 Lys Trp Ile Glu Asn Leu Gln Arg Ala Val Lys Pro Asn Lys Asp Asn
 130 135 140
 agc cgc cgg gta gat aac gtg ctg aaa cta tgg atc ata gaa gct cga 480
 Ser Arg Arg Val Asp Asn Val Leu Lys Leu Trp Ile Ile Glu Ala Arg
 145 150 155
 gag ctg ccc ccc aag aag cga tat tac tgc gag tta tgc ctg gac gac 528
 Glu Leu Pro Pro Lys Lys Arg Tyr Tyr Cys Glu Leu Cys Leu Asp Asp
 160 165 170 175

atg ctc tat gca cgg acc act tcc aag ccc cgc tca gcc tca gga gac Met Leu Tyr Ala Arg Thr Thr Ser Lys Pro Arg Ser Ala Ser Gly Asp 180 185 190	576
act gtc ttt tgg ggc gag cac ttc gag ttt aac aac ctg cct gct gtc Thr Val Phe Trp Gly Glu His Phe Glu Phe Asn Asn Leu Pro Ala Val 195 200 205	624
cgg gcg ctg cgg ctg cat ctg tac cgt gac tcg gac aaa aag cgg aag Arg Ala Leu Arg Leu His Leu Tyr Arg Asp Ser Asp Lys Lys Arg Lys 210 215 220	672
aag gac aag gca ggc tac gtt ggc ctg gtg act gtt cca gtg gcc acc Lys Asp Lys Ala Gly Tyr Val Gly Leu Val Thr Val Pro Val Ala Thr 225 230 235	720
ctg gct ggg cgc cac ttc aca gag cag tgg tac ccc gtg acc ctg cca Leu Ala Gly Arg His Phe Thr Glu Gln Trp Tyr Pro Val Thr Leu Pro 240 245 250 255	768
aca gga agt ggg ggc tct ggg ggt atg ggc tcg ggg gga gga ggg ggg Thr Gly Ser Gly Gly Ser Gly Gly Met Gly Ser Gly Gly Gly Gly Gly 260 265 270	816
tca ggg ggc ggc tca ggg ggc aaa ggg aaa gga ggc tgt cct gct gtg Ser Gly Gly Gly Ser Gly Gly Lys Gly Lys Gly Gly Cys Pro Ala Val 275 280 285	864
cgg ctg aag gcc cgt tac cag aca atg agt atc ctg ccc atg gag cta Arg Leu Lys Ala Arg Tyr Gln Thr Met Ser Ile Leu Pro Met Glu Leu 290 295 300	912
tat aag gag ttt gca gaa tat gtg acc aac cac tac cgc atg ctg tgt Tyr Lys Glu Phe Ala Glu Tyr Val Thr Asn His Tyr Arg Met Leu Cys 305 310 315	960
gcc gtg ctg gag ccc gcc ctc aat gtc aag ggc aag gag gag gtc gct Ala Val Leu Glu Pro Ala Leu Asn Val Lys Gly Lys Glu Glu Val Ala 320 325 330 335	1008
agt gca ctg gtt cac atc ctg caa agc aca ggc aag gcc aag gac ttc Ser Ala Leu Val His Ile Leu Gln Ser Thr Gly Lys Ala Lys Asp Phe 340 345 350	1056
ctt tca gac atg gcc atg tca gag gta gac cgg ttc atg gag cgg gaa Leu Ser Asp Met Ala Met Ser Glu Val Asp Arg Phe Met Glu Arg Glu 355 360 365	1104
cac ctc ata ttc cgc gag aac acg ctc gcc act aaa gcc ata gaa gag His Leu Ile Phe Arg Glu Asn Thr Leu Ala Thr Lys Ala Ile Glu Glu 370 375 380	1152
tat atg aga ctg att ggc cag aaa tac ctc aag gat gcc att ggg gag Tyr Met Arg Leu Ile Gly Gln Lys Tyr Leu Lys Asp Ala Ile Gly Glu 385 390 395	1200

ttc atc cgg gct ctg tat gaa tct gag gag aac tgt gaa gta gac ccc Phe Ile Arg Ala Leu Tyr Glu Ser Glu Glu Asn Cys Glu Val Asp Pro 400 405 410 415	1248
atc aag tgc aca gcg tcc agt ctg gca gag cac cag gcc aac ctg cgg Ile Lys Cys Thr Ala Ser Ser Leu Ala Glu His Gln Ala Asn Leu Arg 420 425 430	1296
atg tgc tgt gag ttg gcc ctg tgc aag gtg gtc aac tcc cat tgc gtg Met Cys Cys Glu Leu Ala Leu Cys Lys Val Val Asn Ser His Cys Val 435 440 445	1344
ttc ccg agg gag ctg aag gag gtg ttt gca tca tgg cgg ctg cgc tgt Phe Pro Arg Glu Leu Lys Glu Val Phe Ala Ser Trp Arg Leu Arg Cys 450 455 460	1392
gca gag cgg ggc cgg gag gac att gct gac agg ctg atc agc gcc tcg Ala Glu Arg Gly Arg Glu Asp Ile Ala Asp Arg Leu Ile Ser Ala Ser 465 470 475	1440
ctc ttc ctg cgc ttc ctc tgc ccg gcc atc atg tcg ccc agt ctg ttt Leu Phe Leu Arg Phe Leu Cys Pro Ala Ile Met Ser Pro Ser Leu Phe 480 485 490 495	1488
gga ctg atg cag gag tac cca gat gag cag acc tca cga acc ctc acc Gly Leu Met Gln Glu Tyr Pro Asp Glu Gln Thr Ser Arg Thr Leu Thr 500 505 510	1536
ctc atc gcc aag gtt atc cag aac ctg gcc aac ttt tcc aag ttt acc Leu Ile Ala Lys Val Ile Gln Asn Leu Ala Asn Phe Ser Lys Phe Thr 515 520 525	1584
tca aag gag gac ttc ctg ggc ttc atg aac gag ttt ctg gag ctg gaa Ser Lys Glu Asp Phe Leu Gly Phe Met Asn Glu Phe Leu Glu Leu Glu 530 535 540	1632
tgg ggt tct atg cag caa ttc ttg tat gag ata tcc aac ctg gac aca Trp Gly Ser Met Gln Gln Phe Leu Tyr Glu Ile Ser Asn Leu Asp Thr 545 550 555	1680
ctg acc aac agc agc agt ttt gag ggc tac ata gac ttg ggc cgc gag Leu Thr Asn Ser Ser Ser Phe Glu Gly Tyr Ile Asp Leu Gly Arg Glu 560 565 570 575	1728
ctc tcc aca ctt cac gcc ctg ctc tgg gag gtg ctg ccc cag ctc agc Leu Ser Thr Leu His Ala Leu Leu Trp Glu Val Leu Pro Gln Leu Ser 580 585 590	1776
aag gaa gcc ctc ctg aag ctg ggc ccg ctg ccc cgg ctc ctc agc gac Lys Glu Ala Leu Leu Lys Leu Gly Pro Leu Pro Arg Leu Leu Ser Asp 595 600 605	1824
atc agc aca gcc ctg agg aac cct aac atc caa agg cag ccg agc cgc Ile Ser Thr Ala Leu Arg Asn Pro Asn Ile Gln Arg Gln Pro Ser Arg 610 615 620	1872

cag agc gag cgc gct cgg tct cag ccc atg gtg ctg cgc ggg ccg tca Gln Ser Glu Arg Ala Arg Ser Gln Pro Met Val Leu Arg Gly Pro Ser 625 630 635	1920
gcc gaa atg cag ggc tac atg atg cgg gac ctc aac agc tcc atc gac Ala Glu Met Gln Gly Tyr Met Met Arg Asp Leu Asn Ser Ser Ile Asp 640 645 650 655	1968
ctt cag tcc ttc atg gct cga ggc ctc aac agc tct atg gac atg gct Leu Gln Ser Phe Met Ala Arg Gly Leu Asn Ser Ser Met Asp Met Ala 660 665 670	2016
cgc ctc ccc tcc cca acc aag gag aaa ccc ccg ccg ccc cct ccc ggt Arg Leu Pro Ser Pro Thr Lys Glu Lys Pro Pro Pro Pro Pro Gly 675 680 685	2064
ggg ggt aaa gac ctg ttc tat gtg agc cgg cca cca ctg gcc cgg tcc Gly Gly Lys Asp Leu Phe Tyr Val Ser Arg Pro Pro Leu Ala Arg Ser 690 695 700	2112
tcc cca gca tac tgc acg agc agc tcg gac atc aca gag ccg gag cag Ser Pro Ala Tyr Cys Thr Ser Ser Ser Asp Ile Thr Glu Pro Glu Gln 705 710 715	2160
aag atg ctg agt gtc aac aag agt gtg tcc atg ctg gac ctg cag ggc Lys Met Leu Ser Val Asn Lys Ser Val Ser Met Leu Asp Leu Gln Gly 720 725 730 735	2208
gac ggg cct ggg ggc cgc ctt aac agc agt agt gtt tcc aac ctg gca Asp Gly Pro Gly Gly Arg Leu Asn Ser Ser Ser Val Ser Asn Leu Ala 740 745 750	2256
gct gtt ggg gac ctg ttg cac tca agc cag gct tca ctg aca gca gcc Ala Val Gly Asp Leu Leu His Ser Ser Gln Ala Ser Leu Thr Ala Ala 755 760 765	2304
ttg ggg ttg cgg cct gca cct gcc ggg cgc ctc tcc caa ggg agt ggc Leu Gly Leu Arg Pro Ala Pro Ala Gly Arg Leu Ser Gln Gly Ser Gly 770 775 780	2352
tct tcc atc aca gca gcc ggc atg cgc ctc agc cag atg ggt gtc act Ser Ser Ile Thr Ala Ala Gly Met Arg Leu Ser Gln Met Gly Val Thr 785 790 795	2400
acg gat ggt gtc ccc gcc cag caa ctg cgc atc cct ctt tcc ttc cag Thr Asp Gly Val Pro Ala Gln Gln Leu Arg Ile Pro Leu Ser Phe Gln 800 805 810 815	2448
aac cct ctc ttc cat atg gct gcc gat gga cca ggg ccc cca gca ggc Asn Pro Leu Phe His Met Ala Ala Asp Gly Pro Gly Pro Pro Ala Gly 820 825 830	2496
cat gga ggg agc agt ggc cat ggt cca cct tcc tcc cat cac cac cac His Gly Gly Ser Ser Gly His Gly Pro Pro Ser Ser His His His His 835 840 845	2544

cac cac cat cac cat cac cga ggg gga gaa ccc cca ggg gac act ttt His His His His His His Arg Gly Gly Glu Pro Pro Gly Asp Thr Phe 850 855 860	2592
gcc ccg ttc cat ggc tat agc aag agc gag gac ctc tct aca ggg gtc Ala Pro Phe His Gly Tyr Ser Lys Ser Glu Asp Leu Ser Thr Gly Val 865 870 875	2640
cct aag ccc cct gcg gcc tcc atc ctt cac agc cac agc tac agt gat Pro Lys Pro Pro Ala Ser Ile Leu His Ser His Ser Tyr Ser Asp 880 885 890 895	2688
gag ttt gga ccc tct ggt act gat ttt acc cgt cgg cag ctc tca ctt Glu Phe Gly Pro Ser Gly Thr Asp Phe Thr Arg Arg Gln Leu Ser Leu 900 905 910	2736
cag gac aac cta cag cac atg ctc tcc ccg ccc cag atc acc atc ggt Gln Asp Asn Leu Gln His Met Leu Ser Pro Pro Gln Ile Thr Ile Gly 915 920 925	2784
ccc cag agg cca gct ccc tca ggg cca gga ggg ggc agt ggt ggg ggc Pro Gln Arg Pro Ala Pro Ser Gly Pro Gly Gly Gly Ser Gly Gly Gly 930 935 940	2832
agt ggt ggg ggc ggt ggg ggc cag cca cct ccc ttg cag agg ggc aaa Ser Gly Gly Gly Gly Gly Gly Gln Pro Pro Pro Leu Gln Arg Gly Lys 945 950 955	2880
tct cag cag ttg aca gtg agt gct gcc cag aaa ccc cgg ccg tcc agc Ser Gln Gln Leu Thr Val Ser Ala Ala Gln Lys Pro Arg Pro Ser Ser 960 965 970 975	2928
ggg aac cta ttg cag tcc ccg gaa cca agt tat ggt cct gcc cgt cca Gly Asn Leu Leu Gln Ser Pro Glu Pro Ser Tyr Gly Pro Ala Arg Pro 980 985 990	2976
cgg caa cag agc ctc agc aaa gag ggc agc att ggg ggc agc ggg ggc Arg Gln Gln Ser Leu Ser Lys Glu Gly Ser Ile Gly Gly Ser Gly Gly 995 1000 1005	3024
agc ggt ggc gga ggg ggt ggg ggg ctc aag ccc tcc atc acc aag cag Ser Gly Gly Gly Gly Gly Gly Gly Leu Lys Pro Ser Ile Thr Lys Gln 1010 1015 1020	3072
cat tcc cag act cca tcc acg ctg aac ccc acg atg ccg gcc tcg gag His Ser Gln Thr Pro Ser Thr Leu Asn Pro Thr Met Pro Ala Ser Glu 1025 1030 1035	3120
cgg act gta gcc tgg gtg tcc aat atg cct cac ctg tcc gct gac atc Arg Thr Val Ala Trp Val Ser Asn Met Pro His Leu Ser Ala Asp Ile 1040 1045 1050 1055	3168
gag agt gca cac att gag cgg gaa gag tac aag ctg aag gag tac tcg Glu Ser Ala His Ile Glu Arg Glu Glu Tyr Lys Leu Lys Glu Tyr Ser 1060 1065 1070	3216

aag tcc atg gac gag agc cga ctg gac agg gtg aag gag tac gag gag Lys Ser Met Asp Glu Ser Arg Leu Asp Arg Val Lys Glu Tyr Glu Glu 1075 1080 1085	3264
gag atc cac tca ctg aag gaa agg cta cac atg tcc aac cgg aag ctg Glu Ile His Ser Leu Lys Glu Arg Leu His Met Ser Asn Arg Lys Leu 1090 1095 1100	3312
gaa gag tac gag cgg agg ctg ctg tcc cag gaa gag cag acc agc aag Glu Glu Tyr Glu Arg Arg Leu Leu Ser Gln Glu Glu Gln Thr Ser Lys 1105 1110 1115	3360
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agg ctg atg ctg gtg gag gag gag ctg cgc cgg gac cac ccc gcc atg Arg Leu Met Leu Val Glu Glu Glu Leu Arg Arg Asp His Pro Ala Met 1155 1160 1165	3504
gct gag ccg ctg cct gaa ccc aag aag agg ctg ctc gac gct cag aga Ala Glu Pro Leu Pro Glu Pro Lys Lys Arg Leu Leu Asp Ala Gln Arg 1170 1175 1180	3552
ggc agc ttc ccc cct tgg gtc caa caa acc cgc gtg tga cgc tgg ccc Gly Ser Phe Pro Pro Trp Val Gln Gln Thr Arg Val Arg Trp Pro 1185 1190 1195	3600
cac ctt gga acg gcc tgg ccc ccc cag ccc cac ccc ccc cac ccc ggc His Leu Gly Thr Ala Trp Pro Pro Gln Pro His Pro Pro His Pro Gly 1200 1205 1210	3648
tgc aga tca cag aga acg gcg agt tcc gga aca ccg cag acc act agc Cys Arg Ser Gln Arg Thr Ala Ser Ser Gly Thr Pro Gln Thr Thr Ser 1215 1220 1225 1230	3696
cca ccc agc atc aca gac ctc ctt ccc tgt gca ccc tac ccc ggc cca Pro Pro Ser Ile Thr Asp Leu Leu Pro Cys Ala Pro Tyr Pro Gly Pro 1235 1240 1245	3744
ccc agc gtc aca gac ctc ctt ccc agt gca ccc gac cct gga aca tca Pro Ser Val Thr Asp Leu Leu Pro Ser Ala Pro Asp Pro Gly Thr Ser 1250 1255 1260	3792
cca acc acc agg act gga cgt cac caa ggg aca gcg gga ttg tct ccc Pro Thr Thr Arg Thr Gly Arg His Gln Gly Thr Ala Gly Leu Ser Pro 1265 1270 1275	3840
tta acg cct cct tgg ggc acc cat ctg tca acc cca ctg ctc cat tcc Leu Thr Pro Pro Trp Gly Thr His Leu Ser Thr Pro Leu Leu His Ser 1280 1285 1290	3888

agg agg gag agt ggg acc ctc agc tgc cct ctc acc cca gga cac cac 3936
 Arg Arg Glu Ser Gly Thr Leu Ser Cys Pro Leu Thr Pro Gly His His
 1295 1300 1305 1310

cta ccc cac aca gac ccc ttc act ctg ggg tgc tat ccc cat cct 3981
 Leu Pro His Thr Asp Pro Phe Thr Leu Gly Cys Tyr Pro His Pro
 1315 1320 1325

<210> 6

<211> 1325

<212> PRT

<213> Unknown Organism

<220>

<223> Description of Unknown Organism: mammalian
 SYNGAP-C

<400> 6

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Gln Gly Phe Leu Ser Arg Arg Leu Lys Ser Ser Ile Lys Arg Thr Lys
 20 25 30

Ser Gln Pro Lys Leu Asp Arg Thr Ser Ser Phe Arg Gln Ile Leu Pro
 35 40 45

Arg Phe Arg Ser Ala Asp His Asp Arg Ala Arg Leu Met Gln Ser Phe
 50 55 60

Lys Glu Ser His Ser His Glu Ser Leu Leu Ser Pro Ser Ser Ala Ala
 65 70 75 80

Glu Ala Leu Glu Leu Asn Leu Asp Glu Asp Ser Ile Ile Lys Pro Val
 85 90 95

His Ser Ser Ile Leu Gly Gln Glu Phe Cys Phe Glu Val Thr Thr Ser
 100 105 110

Ser Gly Thr Lys Cys Phe Ala Cys Arg Ser Ala Ala Glu Arg Asp Lys
 115 120 125

Trp Ile Glu Asn Leu Gln Arg Ala Val Lys Pro Asn Lys Asp Asn Ser
 130 135 140

Arg Arg Val Asp Asn Val Leu Lys Leu Trp Ile Ile Glu Ala Arg Glu
 145 150 155 160

Leu Pro Pro Lys Lys Arg Tyr Tyr Cys Glu Leu Cys Leu Asp Asp Met
 165 170 175

Leu Tyr Ala Arg Thr Thr Ser Lys Pro Arg Ser Ala Ser Gly Asp Thr
 180 185 190

Val Phe Trp Gly Glu His Phe Glu Phe Asn Asn Leu Pro Ala Val Arg
 195 200 205

Ala Leu Arg Leu His Leu Tyr Arg Asp Ser Asp Lys Lys Arg Lys Lys
 210 215 220
 Asp Lys Ala Gly Tyr Val Gly Leu Val Thr Val Pro Val Ala Thr Leu
 225 230 235 240
 Ala Gly Arg His Phe Thr Glu Gln Trp Tyr Pro Val Thr Leu Pro Thr
 245 250 255
 Gly Ser Gly Gly Ser Gly Gly Met Gly Ser Gly Gly Gly Gly Gly Ser
 260 265 270
 Gly Gly Gly Ser Gly Gly Lys Gly Lys Gly Gly Cys Pro Ala Val Arg
 275 280 285
 Leu Lys Ala Arg Tyr Gln Thr Met Ser Ile Leu Pro Met Glu Leu Tyr
 290 295 300
 Lys Glu Phe Ala Glu Tyr Val Thr Asn His Tyr Arg Met Leu Cys Ala
 305 310 315 320
 Val Leu Glu Pro Ala Leu Asn Val Lys Gly Lys Glu Glu Val Ala Ser
 325 330 335
 Ala Leu Val His Ile Leu Gln Ser Thr Gly Lys Ala Lys Asp Phe Leu
 340 345 350
 Ser Asp Met Ala Met Ser Glu Val Asp Arg Phe Met Glu Arg Glu His
 355 360 365
 Leu Ile Phe Arg Glu Asn Thr Leu Ala Thr Lys Ala Ile Glu Glu Tyr
 370 375 380
 Met Arg Leu Ile Gly Gln Lys Tyr Leu Lys Asp Ala Ile Gly Glu Phe
 385 390 395 400
 Ile Arg Ala Leu Tyr Glu Ser Glu Glu Asn Cys Glu Val Asp Pro Ile
 405 410 415
 Lys Cys Thr Ala Ser Ser Leu Ala Glu His Gln Ala Asn Leu Arg Met
 420 425 430
 Cys Cys Glu Leu Ala Leu Cys Lys Val Val Asn Ser His Cys Val Phe
 435 440 445
 Pro Arg Glu Leu Lys Glu Val Phe Ala Ser Trp Arg Leu Arg Cys Ala
 450 455 460
 Glu Arg Gly Arg Glu Asp Ile Ala Asp Arg Leu Ile Ser Ala Ser Leu
 465 470 475 480
 Phe Leu Arg Phe Leu Cys Pro Ala Ile Met Ser Pro Ser Leu Phe Gly
 485 490 495
 Leu Met Gln Glu Tyr Pro Asp Glu Gln Thr Ser Arg Thr Leu Thr Leu
 500 505 510

Ile Ala Lys Val Ile Gln Asn Leu Ala Asn Phe Ser Lys Phe Thr Ser
 515 520 525
 Lys Glu Asp Phe Leu Gly Phe Met Asn Glu Phe Leu Glu Leu Glu Trp
 530 535 540
 Gly Ser Met Gln Gln Phe Leu Tyr Glu Ile Ser Asn Leu Asp Thr Leu
 545 550 555 560
 Thr Asn Ser Ser Ser Phe Glu Gly Tyr Ile Asp Leu Gly Arg Glu Leu
 565 570 575
 Ser Thr Leu His Ala Leu Leu Trp Glu Val Leu Pro Gln Leu Ser Lys
 580 585 590
 Glu Ala Leu Leu Lys Leu Gly Pro Leu Pro Arg Leu Leu Ser Asp Ile
 595 600 605
 Ser Thr Ala Leu Arg Asn Pro Asn Ile Gln Arg Gln Pro Ser Arg Gln
 610 615 620
 Ser Glu Arg Ala Arg Ser Gln Pro Met Val Leu Arg Gly Pro Ser Ala
 625 630 635 640
 Glu Met Gln Gly Tyr Met Met Arg Asp Leu Asn Ser Ser Ile Asp Leu
 645 650 655
 Gln Ser Phe Met Ala Arg Gly Leu Asn Ser Ser Met Asp Met Ala Arg
 660 665 670
 Leu Pro Ser Pro Thr Lys Glu Lys Pro Pro Pro Pro Pro Pro Gly Gly
 675 680 685
 Gly Lys Asp Leu Phe Tyr Val Ser Arg Pro Pro Leu Ala Arg Ser Ser
 690 695 700
 Pro Ala Tyr Cys Thr Ser Ser Ser Asp Ile Thr Glu Pro Glu Gln Lys
 705 710 715 720
 Met Leu Ser Val Asn Lys Ser Val Ser Met Leu Asp Leu Gln Gly Asp
 725 730 735
 Gly Pro Gly Gly Arg Leu Asn Ser Ser Ser Val Ser Asn Leu Ala Ala
 740 745 750
 Val Gly Asp Leu Leu His Ser Ser Gln Ala Ser Leu Thr Ala Ala Leu
 755 760 765
 Gly Leu Arg Pro Ala Pro Ala Gly Arg Leu Ser Gln Gly Ser Gly Ser
 770 775 780
 Ser Ile Thr Ala Ala Gly Met Arg Leu Ser Gln Met Gly Val Thr Thr
 785 790 795 800
 Asp Gly Val Pro Ala Gln Gln Leu Arg Ile Pro Leu Ser Phe Gln Asn
 805 810 815

Pro Leu Phe His Met Ala Ala Asp Gly Pro Gly Pro Pro Ala Gly His
 820 825 830
 Gly Gly Ser Ser Gly His Gly Pro Pro Ser Ser His His His His His
 835 840 845
 His His His His His Arg Gly Gly Glu Pro Pro Gly Asp Thr Phe Ala
 850 855 860
 Pro Phe His Gly Tyr Ser Lys Ser Glu Asp Leu Ser Thr Gly Val Pro
 865 870 875 880
 Lys Pro Pro Ala Ala Ser Ile Leu His Ser His Ser Tyr Ser Asp Glu
 885 890 895
 Phe Gly Pro Ser Gly Thr Asp Phe Thr Arg Arg Gln Leu Ser Leu Gln
 900 905 910
 Asp Asn Leu Gln His Met Leu Ser Pro Pro Gln Ile Thr Ile Gly Pro
 915 920 925
 Gln Arg Pro Ala Pro Ser Gly Pro Gly Gly Gly Ser Gly Gly Gly Ser
 930 935 940
 Gly Gly Gly Gly Gly Gly Gln Pro Pro Pro Leu Gln Arg Gly Lys Ser
 945 950 955 960
 Gln Gln Leu Thr Val Ser Ala Ala Gln Lys Pro Arg Pro Ser Ser Gly
 965 970 975
 Asn Leu Leu Gln Ser Pro Glu Pro Ser Tyr Gly Pro Ala Arg Pro Arg
 980 985 990
 Gln Gln Ser Leu Ser Lys Glu Gly Ser Ile Gly Gly Ser Gly Gly Ser
 995 1000 1005
 Gly Gly Gly Gly Gly Gly Gly Leu Lys Pro Ser Ile Thr Lys Gln His
 1010 1015 1020
 Ser Gln Thr Pro Ser Thr Leu Asn Pro Thr Met Pro Ala Ser Glu Arg
 1025 1030 1035 1040
 Thr Val Ala Trp Val Ser Asn Met Pro His Leu Ser Ala Asp Ile Glu
 1045 1050 1055
 Ser Ala His Ile Glu Arg Glu Glu Tyr Lys Leu Lys Glu Tyr Ser Lys
 1060 1065 1070
 Ser Met Asp Glu Ser Arg Leu Asp Arg Val Lys Glu Tyr Glu Glu Glu
 1075 1080 1085
 Ile His Ser Leu Lys Glu Arg Leu His Met Ser Asn Arg Lys Leu Glu
 1090 1095 1100
 Glu Tyr Glu Arg Arg Leu Leu Ser Gln Glu Glu Gln Thr Ser Lys Ile
 1105 1110 1115 1120

Leu Met Gln Tyr Gln Ala Arg Leu Glu Gln Ser Glu Lys Arg Leu Arg
 1125 1130 1135
 Gln Gln Gln Val Glu Lys Asp Ser Gln Ile Lys Ser Ile Ile Gly Arg
 1140 1145 1150
 Leu Met Leu Val Glu Glu Glu Leu Arg Arg Asp His Pro Ala Met Ala
 1155 1160 1165
 Glu Pro Leu Pro Glu Pro Lys Lys Arg Leu Leu Asp Ala Gln Arg Gly
 1170 1175 1180
 Ser Phe Pro Pro Trp Val Gln Gln Thr Arg Val Arg Trp Pro His Leu
 1185 1190 1195 1200
 Gly Thr Ala Trp Pro Pro Gln Pro His Pro Pro His Pro Gly Cys Arg
 1205 1210 1215
 Ser Gln Arg Thr Ala Ser Ser Gly Thr Pro Gln Thr Thr Ser Pro Pro
 1220 1225 1230
 Ser Ile Thr Asp Leu Leu Pro Cys Ala Pro Tyr Pro Gly Pro Pro Ser
 1235 1240 1245
 Val Thr Asp Leu Leu Pro Ser Ala Pro Asp Pro Gly Thr Ser Pro Thr
 1250 1255 1260
 Thr Arg Thr Gly Arg His Gln Gly Thr Ala Gly Leu Ser Pro Leu Thr
 1265 1270 1275 1280
 Pro Pro Trp Gly Thr His Leu Ser Thr Pro Leu Leu His Ser Arg Arg
 1285 1290 1295
 Glu Ser Gly Thr Leu Ser Cys Pro Leu Thr Pro Gly His His Leu Pro
 1300 1305 1310
 His Thr Asp Pro Phe Thr Leu Gly Cys Tyr Pro His Pro
 1315 1320 1325

<210> 7
 <211> 216
 <212> PRT
 <213> Unknown Organism

<220>
 <223> Description of Unknown Organism: mammalian
 SYNGAP-C

<400> 7
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 20 25 30

Thr Lys Ala Ile Glu Glu Tyr Met Arg Leu Ile Gly Gln Lys Tyr Leu
 35 40 45
 Lys Asp Ala Ile Gly Glu Phe Ile Arg Ala Leu Tyr Glu Ser Glu Glu
 50 55 60
 Asn Cys Glu Val Asp Pro Ile Lys Cys Thr Ala Ser Ser Leu Ala Glu
 65 70 75 80
 His Gln Ala Asn Leu Arg Met Cys Cys Glu Leu Ala Leu Cys Lys Val
 85 90 95
 Val Asn Ser His Cys Val Phe Pro Arg Glu Leu Lys Glu Val Phe Ala
 100 105 110
 Ser Trp Arg Leu Arg Cys Ala Glu Arg Gly Arg Glu Asp Ile Ala Asp
 115 120 125
 Arg Leu Ile Ser Ala Ser Leu Phe Leu Arg Phe Leu Cys Pro Ala Ile
 130 135 140
 Met Ser Pro Ser Leu Phe Gly Leu Met Gln Glu Tyr Pro Asp Glu Gln
 145 150 155 160
 Thr Ser Arg Thr Leu Thr Leu Ile Ala Lys Val Ile Gln Asn Leu Ala
 165 170 175
 Asn Phe Ser Lys Phe Thr Ser Lys Glu Asp Phe Leu Gly Phe Met Asn
 180 185 190
 Glu Phe Leu Glu Leu Glu Trp Gly Ser Met Gln Gln Phe Leu Tyr Glu
 195 200 205
 Ile Ser Asn Leu Asp Thr Leu Thr
 210 215

<210> 8
 <211> 218
 <212> PRT
 <213> Rattus norvegicus

<400> 8
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 Met Glu Asp Glu Ala Thr Thr Leu Phe Arg Ala Thr Thr Leu Ala Ser
 20 25 30
 Thr Leu Met Glu Gln Tyr Met Lys Ala Thr Ala Thr Gln Phe Val His
 35 40 45
 His Ala Leu Lys Asp Ser Ile Leu Lys Ile Met Glu Val Gln His Lys
 50 55 60
 Trp Pro Thr Asn Asn Thr Met Arg Thr Arg Val Val Ser Gly Phe Val
 65 70 75 80

Phe Leu Arg Leu Ile Cys Pro Ala Ile Leu Asn Pro Arg Met Phe Asn
 85 90 95
 Ile Ile Ser Asp Ser Pro Ser Pro Ile Ala Ala Arg Thr Leu Thr Leu
 100 105 110
 Val Ala Lys Ser Val Gln Asn Leu Ala Asn Ser Lys Gln Ser Cys Glu
 115 120 125
 Leu Ser Pro Ser Lys Leu Glu Lys Asn Glu Asp Val Asn Thr Asn Leu
 130 135 140
 Ala His Leu Leu Ser Ile Leu Ser Glu Leu Val Glu Lys Ile Phe Met
 145 150 155 160
 Ala Ser Glu Ile Leu Pro Pro Thr Leu Arg Tyr Ile Tyr Gly Cys Leu
 165 170 175
 Gln Lys Ser Leu Val Glu Phe Gly Ala Lys Glu Pro Tyr Met Glu Gly
 180 185 190
 Val Asn Pro Phe Ile Lys Ser Asn Lys His Arg Met Ile Met Phe Leu
 195 200 205
 Asp Glu Leu Gly Asn Val Pro Glu Leu Pro
 210 215

<210> 9
 <211> 219
 <212> PRT
 <213> Homo sapiens

<400> 9
 His Leu Leu Tyr Gln Leu Leu Trp Asn Met Phe Ser Lys Glu Val Glu
 1 5 10 15
 Leu Ala Asp Ser Met Gln Thr Leu Phe Arg Gly Asn Ser Leu Ala Ser
 20 25 30
 Lys Ile Met Thr Phe Cys Phe Lys Val Tyr Gly Ala Thr Tyr Leu Gln
 35 40 45
 Lys Leu Leu Asp Pro Leu Leu Arg Ile Val Ile Thr Ser Ser Asp Trp
 50 55 60
 Gln His Val Ser Phe Glu Val Asp Pro Thr Arg Leu Glu Pro Ser Glu
 65 70 75 80
 Ser Leu Glu Glu Asn Gln Arg Asn Leu Leu Gln Met Thr Glu Lys Phe
 85 90 95
 Phe His Ala Ile Ile Ser Ser Ser Ser Glu Phe Pro Pro Gln Leu Arg
 100 105 110
 Ser Val Cys His Cys Leu Tyr Gln Val Val Ser Gln Arg Phe Pro Gln
 115 120 125

Asn Ser Ile Gly Ala Val Gly Ser Ala Met Phe Leu Arg Phe Ile Asn
 130 135 140
 Pro Ala Ile Val Ser Pro Tyr Glu Ala Gly Ile Leu Asp Lys Lys Pro
 145 150 155 160
 Pro Pro Arg Ile Glu Arg Gly Leu Lys Leu Met Ser Lys Ile Leu Gln
 165 170 175
 Ser Ile Ala Asn His Val Leu Phe Thr Lys Glu Glu His Met Arg Pro
 180 185 190
 Phe Asn Asp Phe Val Lys Ser Asn Phe Asp Ala Ala Arg Arg Phe Phe
 195 200 205
 Leu Asp Ile Ala Ser Asp Cys Pro Thr Ser Asp
 210 215

<210> 10
 <211> 82
 <212> PRT
 <213> Unknown Organism

<220>
 <223> Description of Unknown Organism: mammalian
 SYNGAP-A

<400> 10
 Phe Lys Glu Ser His Ser His Glu Ser Leu Leu Ser Pro Ser Ser Ala
 1 5 10 15
 Ala Glu Ala Leu Glu Leu Asn Leu Asp Glu Asp Ser Ile Lys Lys Pro
 20 25 30
 Val His Ser Ser Ile Leu Gly Gln Glu Phe Cys Phe Glu Val Thr Thr
 35 40 45
 Ser Ser Gly Thr Lys Cys Phe Ala Cys Arg Ser Ala Ala Glu Arg Asp
 50 55 60
 Lys Trp Ile Glu Asn Leu Gln Arg Ala Val Lys Pro Asn Lys Asp Asn
 65 70 75 80
 Ser Arg

<210> 11
 <211> 114
 <212> PRT
 <213> Homo sapiens

<400> 11
 Phe Tyr Lys Asn Ile Val Lys Lys Gly Tyr Leu Leu Lys Lys Gly Lys
 1 5 10 15
 Gly Lys Arg Trp Lys Asn Leu Tyr Phe Ile Leu Glu Gly Ser Asp Ala
 20 25 30

Pro Gly

Met Glu Pro Lys Arg Ile Arg Glu Gly Tyr Leu Val Lys Lys Gly Ser
1 5 10 15

Val Phe Asn Thr Trp Lys Pro Met Trp Val Val Leu Leu Glu Asp Gly
 20 25 30
 Ile Glu Phe Tyr Lys Lys Lys Ser Asp Asn Ser Pro Lys Gly Met Ile
 35 40 45
 Pro Leu Lys Gly Ser Thr Leu Thr Ser Pro Cys Gln Asp Phe Gly Lys
 50 55 60
 Arg Met Phe Val Phe Lys Ile Thr Thr Thr Lys Gln Gln Asp His Phe
 65 70 75 80
 Phe Gln Ala Ala Phe Leu Glu Glu Arg Asp Ala Trp Val Arg Asp Ile
 85 90 95
 Asn Lys Ala Ile Lys Cys Ile Glu Gly Gly Gln Lys
 100 105

<210> 14

<211> 110

<212> PRT

<213> Unknown Organism

<220>

<223> Description of Unknown Organism: mammalian
 SYNGAP-A

<400> 14

Val Asp Asn Val Leu Lys Leu Trp Ile Ile Glu Ala Arg Glu Leu Pro
 1 5 10 15
 Pro Lys Lys Arg Tyr Tyr Cys Glu Leu Cys Leu Asp Asp Met Leu Tyr
 20 25 30
 Ala Arg Thr Thr Ser Lys Pro Arg Ser Ala Ser Gly Asp Thr Val Phe
 35 40 45
 Trp Gly Glu His Phe Glu Phe Asn Asn Leu Pro Ala Val Arg Ala Leu
 50 55 60
 Arg Leu His Leu Tyr Arg Asp Ser Asp Lys Lys Arg Lys Lys Asp Lys
 65 70 75 80
 Ala Gly Tyr Val Gly Leu Val Thr Val Pro Val Ala Thr Leu Ala Gly
 85 90 95
 Arg His Phe Thr Glu Gln Trp Tyr Pro Val Thr Leu Pro Thr
 100 105 110

<210> 15

<211> 107

<212> PRT

<213> Homo sapiens

<400> 15

Gln Val Ser Ser Leu Val Leu His Ile Glu Glu Ala His Lys Leu Pro
 1 5 10 15

Val Lys His Phe Thr Asn Pro Tyr Cys Asn Ile Tyr Leu Asn Ser Val
 20 25 30

Gln Val Ala Lys Thr His Ala Arg Glu Gly Gln Asn Pro Val Trp Ser
 35 40 45

Glu Glu Phe Val Phe Asp Asp Leu Pro Pro Asp Ile Asn Arg Phe Glu
 50 55 60

Ile Thr Leu Ser Asn Lys Thr Lys Lys Ser Lys Asp Pro Asp Ile Leu
 65 70 75 80

Phe Met Arg Cys Gln Leu Ser Arg Leu Gln Lys Gly His Ala Thr Asp
 85 90 95

Glu Trp Phe Leu Leu Ser Ser His Ile Pro Leu
 100 105

<210> 16

<211> 116

<212> PRT

<213> Rattus norvegicus

<400> 16

Asp Tyr Asp Phe Gln Ala Asn Gln Leu Thr Val Gly Val Leu Gln Ala
 1 5 10 15

Ala Glu Leu Pro Ala Leu Asp Met Gly Gly Thr Ser Asp Pro Tyr Val
 20 25 30

Lys Val Phe Leu Leu Pro Asp Lys Lys Lys Lys Tyr Glu Thr Lys Val
 35 40 45

His Arg Lys Thr Leu Asn Pro Ala Phe Asn Glu Thr Phe Thr Phe Lys
 50 55 60

Val Pro Tyr Gln Glu Leu Gly Gly Lys Thr Leu Val Met Ala Ile Tyr
 65 70 75 80

Asp Phe Asp Arg Phe Ser Lys His Asp Ile Ile Gly Glu Val Lys Val
 85 90 95

Pro Met Asn Thr Val Asp Leu Gly Gln Pro Ile Glu Glu Trp Arg Asp
 100 105 110

Leu Gln Gly Gly
 115

<210> 17

<211> 132

<212> PRT

<213> Bos taurus

<400> 17

Leu Tyr Asp Gln Asp Asn Ser Ser Leu Lys Cys Thr Ile Ile Lys Ala
 1 5 10 15

Lys Gly Leu Lys Pro Met Asp Ser Asn Gly Leu Ala Asp Pro Tyr Val
 20 25 30

Lys Leu His Leu Leu Pro Gly Ala Ser Lys Ser Asn Lys Leu Arg Thr
 35 40 45

Lys Thr Leu Arg Asn Thr Arg Asn Pro Ile Trp Asn Glu Thr Leu Val
 50 55 60

Tyr His Gly Ile Thr Asp Glu Asp Met Gln Arg Lys Thr Leu Arg Ile
 65 70 75 80

Ser Val Cys Asp Glu Asp Lys Phe Gly His Asn Glu Phe Ile Gly Glu
 85 90 95

Thr Arg Phe Ser Leu Lys Lys Leu Lys Pro Asn Gln Arg Lys Asn Phe
 100 105 110

Asn Ile Cys Leu Glu Arg Val Ile Pro Met Lys Arg Ala Gly Thr Thr
 115 120 125

Gly Ser Ala Arg
 130

<210> 18

<211> 26

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:
 Oligonucleotide

<400> 18

acgcgtcgac cagagagccc cgcaag

26

<210> 19

<211> 26

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:
 Oligonucleotide

<400> 19

gaagatctag gtctatactg ggccac

26

<210> 20

<211> 20

<212> PRT
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence: Synthetic
 peptide

<400> 20
 Lys Arg Leu Leu Asp Ala Gln Arg Gly Ser Phe Pro Pro Trp Val Gln
 1 5 10 15
 Gln Thr Arg Val
 20

<210> 21
 <211> 1135
 <212> PRT
 <213> Unknown Organism

<220>
 <223> Description of Unknown Organism: mammalian
 SYNGAP-C

<400> 21
 Met Gln Ser Phe Lys Glu Ser His Ser His Glu Ser Leu Leu Ser Pro
 1 5 10 15
 Ser Ser Ala Ala Glu Ala Leu Glu Leu Asn Leu Asp Glu Asp Ser Ile
 20 25 30
 Ile Lys Pro Val His Ser Ser Ile Leu Gly Gln Glu Phe Cys Phe Glu
 35 40 45
 Val Thr Thr Ser Ser Gly Thr Lys Cys Phe Ala Cys Arg Ser Ala Ala
 50 55 60
 Glu Arg Asp Lys Trp Ile Glu Asn Leu Gln Arg Ala Val Lys Pro Asn
 65 70 75 80
 Lys Asp Asn Ser Arg Arg Val Asp Asn Val Leu Lys Leu Trp Ile Ile
 85 90 95
 Glu Ala Arg Glu Leu Pro Pro Lys Lys Arg Tyr Tyr Cys Glu Leu Cys
 100 105 110
 Leu Asp Asp Met Leu Tyr Ala Arg Thr Thr Ser Lys Pro Arg Ser Ala
 115 120 125
 Ser Gly Asp Thr Val Phe Trp Gly Glu His Phe Glu Phe Asn Asn Leu
 130 135 140
 Pro Ala Val Arg Ala Leu Arg Leu His Leu Tyr Arg Asp Ser Asp Lys
 145 150 155 160
 Lys Arg Lys Lys Asp Lys Ala Gly Tyr Val Gly Leu Val Thr Val Pro
 165 170 175

Val Ala Thr Leu Ala Gly Arg His Phe Thr Glu Gln Trp Tyr Pro Val
 180 185 190
 Thr Leu Pro Thr Gly Ser Gly Gly Ser Gly Gly Met Gly Ser Gly Gly
 195 200 205
 Gly Gly Gly Ser Gly Gly Gly Ser Gly Gly Lys Gly Lys Gly Gly Cys
 210 215 220
 Pro Ala Val Arg Leu Lys Ala Arg Tyr Gln Thr Met Ser Ile Leu Pro
 225 230 235 240
 Met Glu Leu Tyr Lys Glu Phe Ala Glu Tyr Val Thr Asn His Tyr Arg
 245 250 255
 Met Leu Cys Ala Val Leu Glu Pro Ala Leu Asn Val Lys Gly Lys Glu
 260 265 270
 Glu Val Ala Ser Ala Leu Val His Ile Leu Gln Ser Thr Gly Lys Ala
 275 280 285
 Lys Asp Phe Leu Ser Asp Met Ala Met Ser Glu Val Asp Arg Phe Met
 290 295 300
 Glu Arg Glu His Leu Ile Phe Arg Glu Asn Thr Leu Ala Thr Lys Ala
 305 310 315 320
 Ile Glu Glu Tyr Met Arg Leu Ile Gly Gln Lys Tyr Leu Lys Asp Ala
 325 330 335
 Ile Gly Glu Phe Ile Arg Ala Leu Tyr Glu Ser Glu Glu Asn Cys Glu
 340 345 350
 Val Asp Pro Ile Lys Cys Thr Ala Ser Ser Leu Ala Glu His Gln Ala
 355 360 365
 Asn Leu Arg Met Cys Cys Glu Leu Ala Leu Cys Lys Val Val Asn Ser
 370 375 380
 His Cys Val Phe Pro Arg Glu Leu Lys Glu Val Phe Ala Ser Trp Arg
 385 390 395 400
 Leu Arg Cys Ala Glu Arg Gly Arg Glu Asp Ile Ala Asp Arg Leu Ile
 405 410 415
 Ser Ala Ser Leu Phe Leu Arg Phe Leu Cys Pro Ala Ile Met Ser Pro
 420 425 430
 Ser Leu Phe Gly Leu Met Gln Glu Tyr Pro Asp Glu Gln Thr Ser Arg
 435 440 445
 Thr Leu Thr Leu Ile Ala Lys Val Ile Gln Asn Leu Ala Asn Phe Ser
 450 455 460
 Lys Phe Thr Ser Lys Glu Asp Phe Leu Gly Phe Met Asn Glu Phe Leu
 465 470 475 480

Glu Leu Glu Trp Gly Ser Met Gln Gln Phe Leu Tyr Glu Ile Ser Asn
 485 490 495
 Leu Asp Thr Leu Thr Asn Ser Ser Ser Phe Glu Gly Tyr Ile Asp Leu
 500 505 510
 Gly Arg Glu Leu Ser Thr Leu His Ala Leu Leu Trp Glu Val Leu Pro
 515 520 525
 Gln Leu Ser Lys Glu Ala Leu Leu Lys Leu Gly Pro Leu Pro Arg Leu
 530 535 540
 Leu Ser Asp Ile Ser Thr Ala Leu Arg Asn Pro Asn Ile Gln Arg Gln
 545 550 555 560
 Pro Ser Arg Gln Ser Glu Arg Ala Arg Ser Gln Pro Met Val Leu Arg
 565 570 575
 Gly Pro Ser Ala Glu Met Gln Gly Tyr Met Met Arg Asp Leu Asn Ser
 580 585 590
 Ser Ile Asp Leu Gln Ser Phe Met Ala Arg Gly Leu Asn Ser Ser Met
 595 600 605
 Asp Met Ala Arg Leu Pro Ser Pro Thr Lys Glu Lys Pro Pro Pro Pro
 610 615 620
 Pro Pro Gly Gly Gly Lys Asp Leu Phe Tyr Val Ser Arg Pro Pro Leu
 625 630 635 640
 Ala Arg Ser Ser Pro Ala Tyr Cys Thr Ser Ser Ser Asp Ile Thr Glu
 645 650 655
 Pro Glu Gln Lys Met Leu Ser Val Asn Lys Ser Val Ser Met Leu Asp
 660 665 670
 Leu Gln Gly Asp Gly Pro Gly Gly Arg Leu Asn Ser Ser Ser Val Ser
 675 680 685
 Asn Leu Ala Ala Val Gly Asp Leu Leu His Ser Ser Gln Ala Ser Leu
 690 695 700
 Thr Ala Ala Leu Gly Leu Arg Pro Ala Pro Ala Gly Arg Leu Ser Gln
 705 710 715 720
 Gly Ser Gly Ser Ser Ile Thr Ala Ala Gly Met Arg Leu Ser Gln Met
 725 730 735
 Gly Val Thr Thr Asp Gly Val Pro Ala Gln Gln Leu Arg Ile Pro Leu
 740 745 750
 Ser Phe Gln Asn Pro Leu Phe His Met Ala Ala Asp Gly Pro Gly Pro
 755 760 765
 Pro Ala Gly His Gly Gly Ser Ser Gly His Gly Pro Pro Ser Ser His
 770 775 780

His	His	His	His	His	His	His	His	His	His	Arg	Gly	Gly	Glu	Pro	Pro	Gly	785	790	795	800
Asp	Thr	Phe	Ala	Pro	Phe	His	Gly	Tyr	Ser	Lys	Ser	Glu	Asp	Leu	Ser		805	810		815
Thr	Gly	Val	Pro	Lys	Pro	Pro	Ala	Ala	Ser	Ile	Leu	His	Ser	His	Ser		820	825		830
Tyr	Ser	Asp	Glu	Phe	Gly	Pro	Ser	Gly	Thr	Asp	Phe	Thr	Arg	Arg	Gln		835	840		845
Leu	Ser	Leu	Gln	Asp	Asn	Leu	Gln	His	Met	Leu	Ser	Pro	Pro	Gln	Ile		850	855		860
Thr	Ile	Gly	Pro	Gln	Arg	Pro	Ala	Pro	Ser	Gly	Pro	Gly	Gly	Gly	Ser		865	870		875
Gly	Gly	Gly	Ser	Gly	Gly	Gly	Gly	Gly	Gly	Gln	Pro	Pro	Pro	Leu	Gln		885	890		895
Arg	Gly	Lys	Ser	Gln	Gln	Leu	Thr	Val	Ser	Ala	Ala	Gln	Lys	Pro	Arg		900	905		910
Pro	Ser	Ser	Gly	Asn	Leu	Leu	Gln	Ser	Pro	Glu	Pro	Ser	Tyr	Gly	Pro		915	920		925
Ala	Arg	Pro	Arg	Gln	Gln	Ser	Leu	Ser	Lys	Glu	Gly	Ser	Ile	Gly	Gly		930	935		940
Ser	Gly	Gly	Ser	Gly	Gly	Gly	Gly	Gly	Gly	Gly	Leu	Lys	Pro	Ser	Ile		945	950		955
Thr	Lys	Gln	His	Ser	Gln	Thr	Pro	Ser	Thr	Leu	Asn	Pro	Thr	Met	Pro		965	970		975
Ala	Ser	Glu	Arg	Thr	Val	Ala	Trp	Val	Ser	Asn	Met	Pro	His	Leu	Ser		980	985		990
Ala	Asp	Ile	Glu	Ser	Ala	His	Ile	Glu	Arg	Glu	Glu	Tyr	Lys	Leu	Lys		995	1000		1005
Glu	Tyr	Ser	Lys	Ser	Met	Asp	Glu	Ser	Arg	Leu	Asp	Arg	Val	Lys	Glu		1010	1015		1020
Tyr	Glu	Glu	Glu	Ile	His	Ser	Leu	Lys	Glu	Arg	Leu	His	Met	Ser	Asn		1025	1030		1035
Arg	Lys	Leu	Glu	Glu	Tyr	Glu	Arg	Arg	Leu	Leu	Ser	Gln	Glu	Glu	Gln		1045	1050		1055
Thr	Ser	Lys	Ile	Leu	Met	Gln	Tyr	Gln	Ala	Arg	Leu	Glu	Gln	Ser	Glu		1060	1065		1070
Lys	Arg	Leu	Arg	Gln	Gln	Gln	Val	Glu	Lys	Asp	Ser	Gln	Ile	Lys	Ser		1075	1080		1085

Ile Ile Gly Arg Leu Met Leu Val Glu Glu Glu Leu Arg Arg Asp His
1090 1095 1100

Pro Ala Met Ala Glu Pro Leu Pro Glu Pro Lys Lys Arg Leu Leu Asp
1105 1110 1115 1120

Ala Gln Arg Gly Ser Phe Pro Pro Trp Val Gln Gln Thr Arg Val
1125 1130 1135

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